

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana White, David MacBeth, Kyle J. <120> 2786, A NOVEL HUMAN AMINOPEPTIDASE <130> MPI99-193CN2M <140> US 10/767,308 <141> 2004-01-29 <150> US 09/443,795 <151> 1999-11-19 <150> US 10/056,253 <151> 2002-01-24 <160> 8 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 650 <212> PRT <213> Homo sapiens <400> 1 Met Ala Ser Gly Glu His Ser Pro Gly Ser Gly Ala Ala Arg Arg Pro 10 Leu His Ser Ala Gln Ala Val Asp Val Ala Ser Ala Ser Asn Phe Arg 25 Ala Phe Glu Leu Leu His Leu His Leu Asp Leu Arg Ala Glu Phe Gly 40 45 Pro Pro Gly Pro Gly Ala Gly Ser Arg Gly Leu Ser Gly Thr Ala Val 55 Leu Asp Leu Arg Cys Leu Glu Pro Glu Gly Ala Ala Glu Leu Arg Leu 70 75 Asp Ser His Pro Cys Leu Glu Val Thr Ala Ala Ala Leu Arg Arg Glu 85 90 Arg Pro Gly Ser Glu Glu Pro Pro Ala Glu Pro Val Ser Phe Tyr Thr 100 105 110 Gln Pro Phe Ser His Tyr Gly Gln Ala Leu Cys Val Ser Phe Pro Gln 120 125 115 Pro Cys Arg Ala Ala Glu Arg Leu Gln Val Leu Leu Thr Tyr Arg Val 135 Gly Glu Gly Pro Gly Val Cys Trp Leu Ala Pro Glu Gln Thr Ala Gly 145 150 155 Lys Lys Lys Pro Phe Val Tyr Thr Gln Gly Gln Ala Val Leu Asn Arg 170 165 Ala Phe Phe Pro Cys Phe Asp Thr Pro Ala Val Lys Tyr Lys Tyr Ser 180 185 190 Ala Leu Ile Glu Val Pro Asp Gly Phe Thr Ala Val Met Ser Ala Ser 195 200 205 Thr Trp Glu Lys Arg Gly Pro Asn Lys Phe Phe Gln Met Cys Gln 215 220 Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser 235 230 Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile

250

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Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val Ile Glu Glu Phe Leu Ala
          260
                               265
Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu
       275
                          280
                                              285
Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys
                      295
                                          300
Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala
                                      315
                  310
Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val
                       330
               325
Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met
                               345
Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr
                           360
                                              365
Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp
                       375
                                         380
Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu
                  390
                                      395
Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys
               405
                                 410
Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp
          420
                               425
Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg
       435
                          440
                                             445
Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro
                      455
                                         460
 450
Glu Leu Lys Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp
                  470
                                      475
Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser
       485
                                 490
Pro Gly Asp Ser Leu Met Lys Pro Ala Glu Glu Leu Ala Gln Leu Trp
                               505
Ala Ala Glu Glu Leu Asp Met Lys Ala Ile Glu Ala Val Ala Ile Ser
       515
                           520
                                              525
Pro Trp Lys Thr Tyr Gln Leu Val Tyr Phe Leu Asp Lys Ile Leu Gln
                       535
                                          540
Lys Ser Pro Leu Pro Pro Gly Asn Val Lys Lys Leu Gly Asp Thr Tyr
                  550
                                      555
Pro Ser Ile Ser Asn Ala Arg Asn Ala Glu Leu Arg Leu Arg Trp Gly
              565
                                  570
                                                      575
Gln Ile Val Leu Lys Asn Asp His Gln Glu Asp Phe Trp Lys Val Lys
                               585
                                                  590
           580
Glu Phe Leu His Asn Gln Gly Lys Gln Lys Tyr Thr Leu Pro Leu Tyr
                                             605
       595
                          600
His Ala Met Met Gly Gly Ser Glu Val Ala Gln Thr Leu Ala Lys Glu
                      615
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Thr Phe Ala Ser Thr Ala Ser Gln Leu His Ser Asn Val Val Asn Tyr
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Val Gln Gln Ile Val Ala Pro Lys Gly Ser
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<223> n = A,T,C or G															
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	cac His														157
	ttt Phe														205
	cca Pro 50				_									_	253
	gac Asp														301
	tcg Ser														349
	ccc Pro														397
	ccc Pro														445
	tgc Cys 130														493
	gag Glu														541
	aag Lys														589
	ttc Phe														637
	ctt Leu														685
	tgg Trp 210														733

ccc atc ccc tcc tat ctg ata gct ttg gcc atc gga gat ctg gtt tcg 781

	Pro 225	Ile	Pro	Ser	Tyr	Leu 230	Ile	Ala	Leu	Ala	11e 235	Gly	Asp	Leu	Val	Ser 240		
	_	-	_					cgg Arg									829	
								aac Asn									877	
								cct Pro 280									925	
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								ctg Leu									1021	
								tcc Ser									1069	
								ttc Phe									1117	
		_	_					acc Thr 360									1165	
٠								cgg Arg									1213	
								ctc Leu									1261	
								acc Thr									1309	
			_		_			ctg Leu	_		_			_	-		1357	
	_		_	-			_	gcc Ala 440				_					1405	
								ctg Leu									1453	
	gag Glu 465	ctt Leu	aag Lys	aaa Lys	aag Lys	aga Arg 470	gtg Val	gat Asp	atc Ile	att Ile	cca Pro 475	ggt Gly	ttt Phe	gag Glu	ttt Phe	gat Asp 480	1501	

		_							ccg Pro 490							1549
									gaa Glu							1597
									att Ile							1645
									ttc Phe							1693
									aaa Lys					_		1741
									gag Glu 570							1789
		_		_		_		_	gaa Glu	-						1837
		_			_				aag Lys		_					1885
	-	-	_			-			gcc Ala	_			_			1933
		-			_		_		cac His	-		_	_			1981
_	-	-			gca Ala				agt Ser 650	taga	aggct	cg t	gtgo	catgo	ic	2031
cctg ctgt gaga ggta tttc tttt aaaa	gatca gact icaga ittct itctt ittca iaaaa	ac to tage according to the tage to take the tage to take tage tage tage tage tage tage tage tag	teet gggg acctg cccc	ggag ectet gecea eacet ettt	gt tt g ct ac ag ta ag	atat ctgg gctct gtctc tgct	cccc gtggg cccc ctggg cgatt	tca g aac g gct g aac tta	aggat ettac eacag gaagt atgca	taat ette gget egga aaag	ctat tcta gcag gagg	tcto atago ggcao gacto ggca	cta g ccc a ctg d gat g att d	gctta actga caggg gctct ctgat	etgtte aggtat agecee geageg etettt etgtte aaaaaa	2091 2151 2211 2271 2331 2391 2451 2459

<211> 30 <212> PRT

<213> Artificial Sequence

<220>

<223> Ribonucleoprotein Binding Site

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Gly Ser Cys Ile Phe Tyr Leu Ile Val Ala Xaa Phe Tyr Met
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                                25
<210> 4
<211> 3
<212> PRT
<213> Artificial Sequence
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<223> Nuclear Localization Motif
<400> 4
Lys Lys Lys
<210> 5
<211> 8
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Lys Gly Tyr Cys Phe Val Ser Tyr
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<212> PRT
<213> Artificial Sequence
<223> potential catalytic site
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His Glu Ile Ser His
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<211> 4
<212> PRT
<213> Artificial Sequence
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<223> potential catalytic site
<400> 7
Trp Leu Asn Glu
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1